



1/36

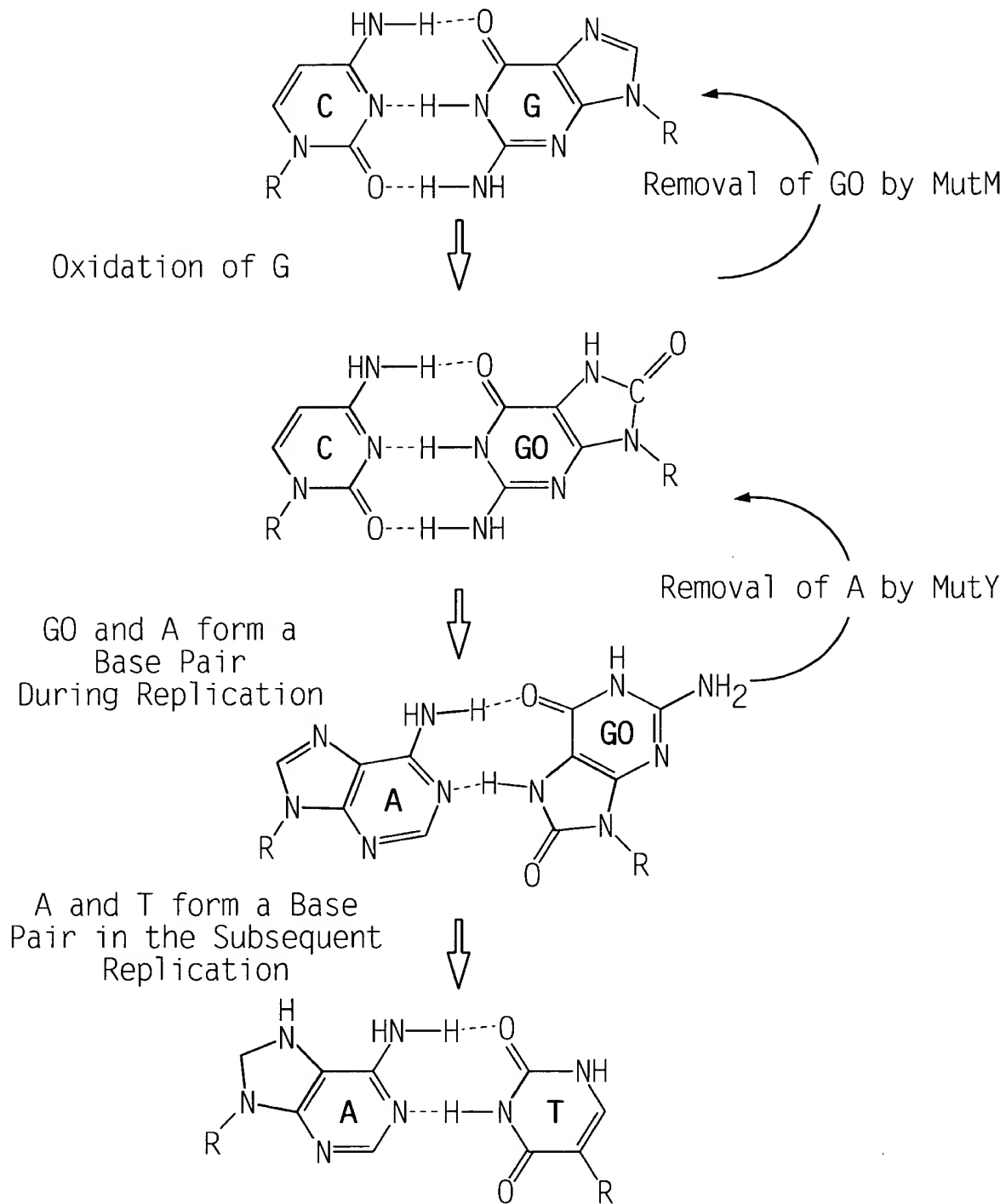
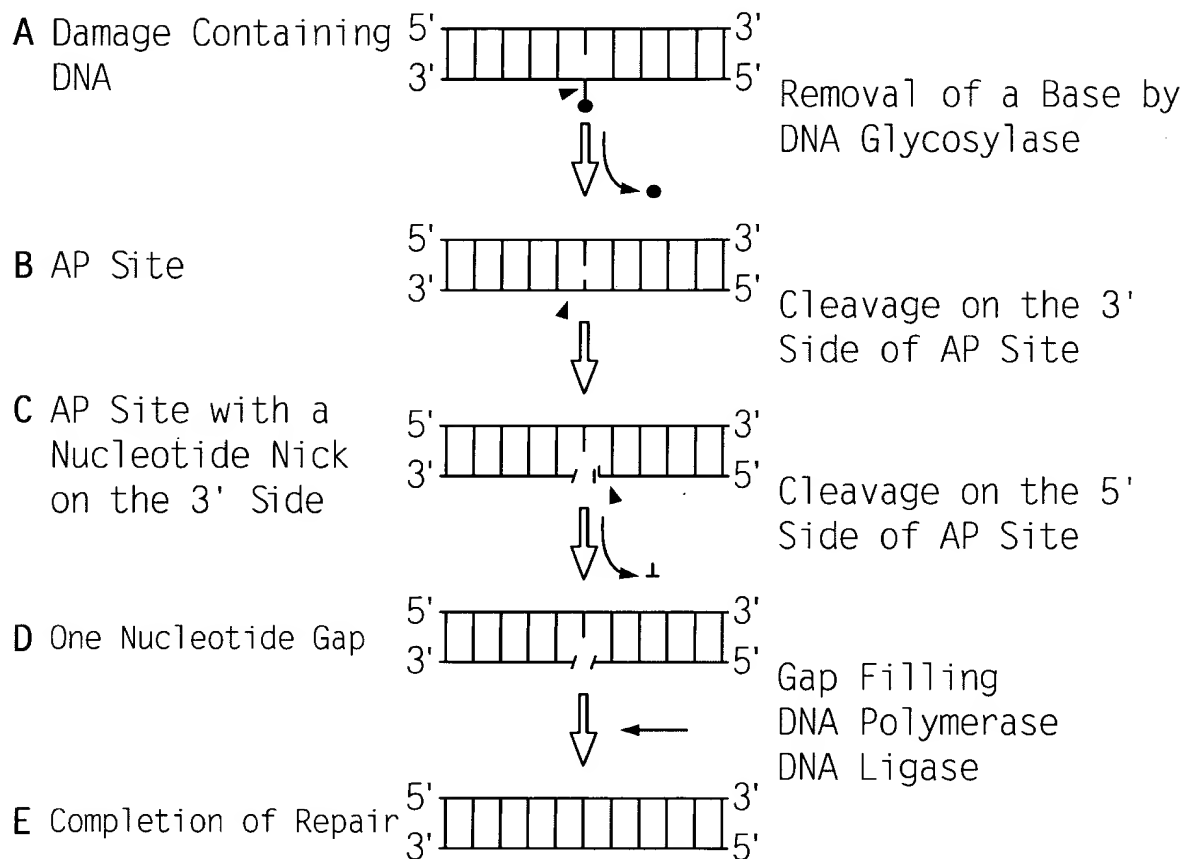


FIG. 1



2/36



**FIG. 2**



3/36

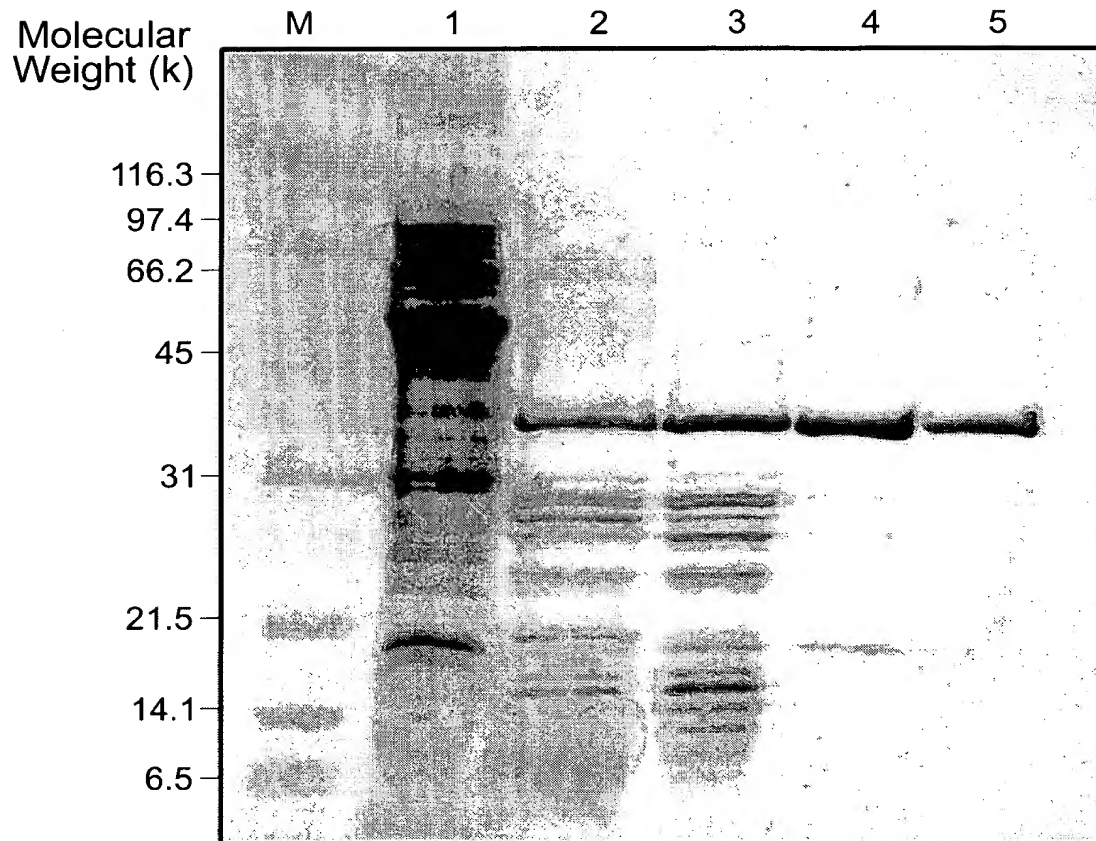


FIG. 3



4/36

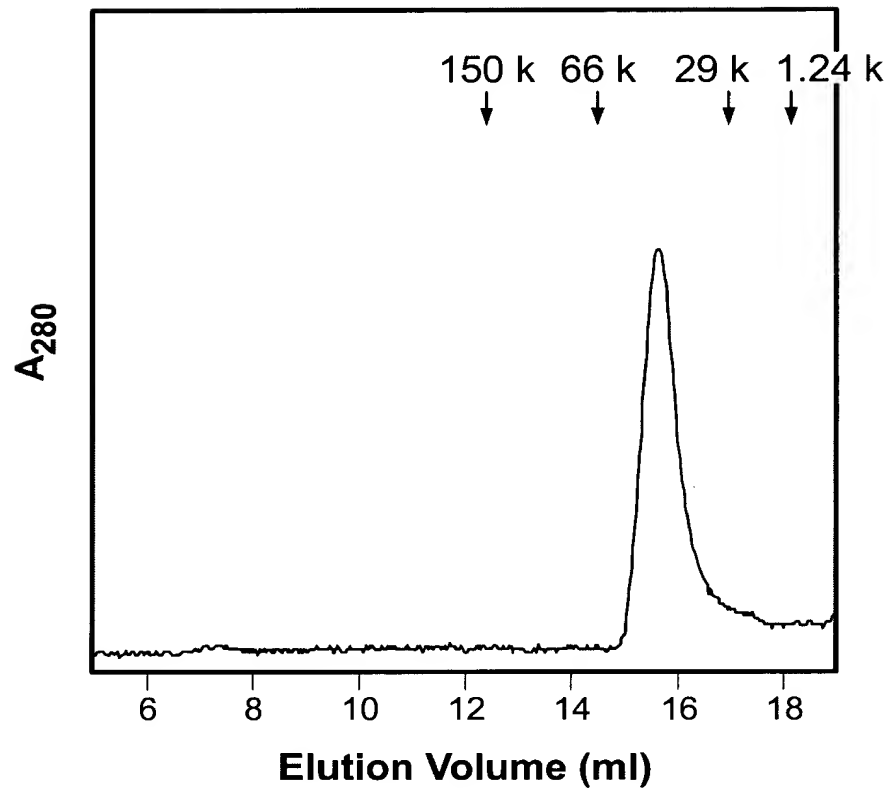


FIG. 4



5/36

Tth MutY	1	MEAWRKALAWREN-ARPLPWR	GE	KDPIRRLVSEMLQOTRWEQALPIYRRFL	53
Hsa MutY	51	CDGLARQPEEVVLQASVSYHLFRDVAEVTAFRGSLSWDOE-KRDLPARRRAEDMDLD		RRAYANWSEVMLQOTQWATVILNYITGMM	139
Spo MutY	1	MSDSNHFLDLHSYTQLEVERFRESLIDFYDKT-KRIIPARKKECIPPSSEDSPLDWEQPVQRVRLYEMVSEMLQOTRWEITVKRYITKMM			88
Eco MutY	1	MQASQFSQAQVLDWDYKGRKTLPMD	ID	KTPYKQMLSEVMLQOTQWATVILPIYFERFM	56
Eco EndoIII	1	MNKAKRLLELLRLREN--NPHTT	ELN	FSSPFELLIAVLLSAQATDVSYNKATAKLY	55
Tth MutY	54	ERFPITIKALAAASLE-EVLRMQAGAYR-RAEHLHRLARSVEEL-----PPSFAELR-GPGGPTYAAVAVASI AFGERVAADVGNVRRVLSRLFAR			145
Hsa MutY	140	QKWPITLQDLASASLE-EVNQLWAGLGYYS-RGRRLDEGARKVVEELGGHMPRTAE TLQQLPGVGRYTAGAIASI AFQDATGVVDGNVARVLCRRVRLGA			237
Spo MutY	89	ETLPTIKSCAEAEYNTQWPLWSGMGFYT-RCKRLHQACQHLAKLHPSEIPRTGDEMAGGLPGVGPYTAGAVLSI AWKOPTGI VDGNVILRVLSRALAH			187
Eco MutY	57	ARFPITIDLANAPLD-EVLHLMTGLGYA-RARNLHKAADQVATLHGGKPEITFEEMA-ALPGVGRSTAGAILSLGKHFPITLDGNIKRVLCRCYANSG			153
Eco EndoIII	56	PVANTPAAMLELGMF-GVKTYIKTIGLYNSKAENIKTCRI LLEQHNGEVPEDRAALF-ALPGVGRKTAANVINTAFGWPITIAVDTHIFRVCNRTQFAPG			153
Tth MutY	146	-PK-----EKELFWLAQGLPEGVDPGVWNOALMELGATVCLPKRPRCGACPTLGAFCRG-----KEAPGRYP-----APR-----			K 210
Hsa MutY	238	DPSSLVSOQLWGLAQQLMDP-ARPGDFNOAMMELGATVCTPQRPLCSQCPVE SLCRARQVEQEQLLASGSLSGSPDVEECAPNTGQCHLCLPPSEPM			336
Spo MutY	188	DCSKGKANALLWKLANELMDP-VRPGDFNOALMELGALTCTPQSPRCSVCPITSEICKAYQ---EQNVIRDGNITIKYD--TEDVPCN-ICITDIPS---			K 276
Eco MutY	154	MPGKKEVENKLWLSLSEQVTPA-VGVERFNOAMMDLGAMICTRSKPKCSLOPLNGCIA-----AANNSWALYP-----GKK-----			P 225
Eco EndoIII	154	-KN-----VEQFEKLLKWWPA-EFKVDCHHLLHGRYTCTIARKKRCGSCITLEDLCEY-----			205
Tth MutY	211	RRAK-----EER--LVALVLLGRKG-----VHLERLEGR-----FQGLGVDFPFP-EP-GRFAFGVRS-----RP-----			L 266
Hsa MutY	337	QTLGV---VNFPRKASRKPREESSATCVLEQPGA---LGAQILLVORPNSGLAGLMEFDSVTW-EPSELQQRKIALQELQRWAGP-----LPATLRLHL			425
Spo MutY	277	EDLQNWVVARYPVHPAKTKQRE-ERALVWTFQKTDPSKKEFFLLPKRPSAGLLAGLWDFPTIEFGQESMPKQMDAEFKQSI AQWISNDSRSLIKKYQSR			375
Eco MutY	226	QTL-----PER---TGYFLLLOH-----EDEVLLACRPPSGLMGGLYCFDPADEES- LQWL AQQR-----LRQWL AQQR-----			I AADNL TQL 287
Eco EndoIII	206	--K-----EKVDI			
Tth MutY	267	GEVRHALLTHRLR-----VEVR-GALWEGEEDPWKRPP--LPKLMKMLRKALP-----LAH-----			AGVPLPDA 325
Hsa MutY	426	GEVWHIFSHIKLTYQVYGLALEGQTPVTTPPGARMLTOEEFHTAAVSTAMKKVFRMYDGGQDGTGCKGSRQSVSSPSRKKPRMGQQVLDNFFRSHISIDAHSLNSAAQ			535
Spo MutY	376	GRYLHIFSHIRKTSHVFYAIAS---PDIVTINEDFFMISSDLEHVGMC---ELGLKNVRALEIKKRK-----VTSLSN-----			FKEPKLTSARLIVTKAEC 461
Eco MutY	288	TAFRHIFSHFHLD-----IIP---MMLPVSSFTGCMDE-----EGNALWNLNADP-PSVG-----LAADVER-----			LLQLRLGAPV 350

Tth (Thermus thermophilus HBB), Hsa (Homo sapiens), Spo (Schizosaccharomyces pombe), Eco (Escherichia coli)  
# Residue essential for N-glycosylase activity \* Residues constituting an iron-sulfur cluster

FIG. 5



6/36

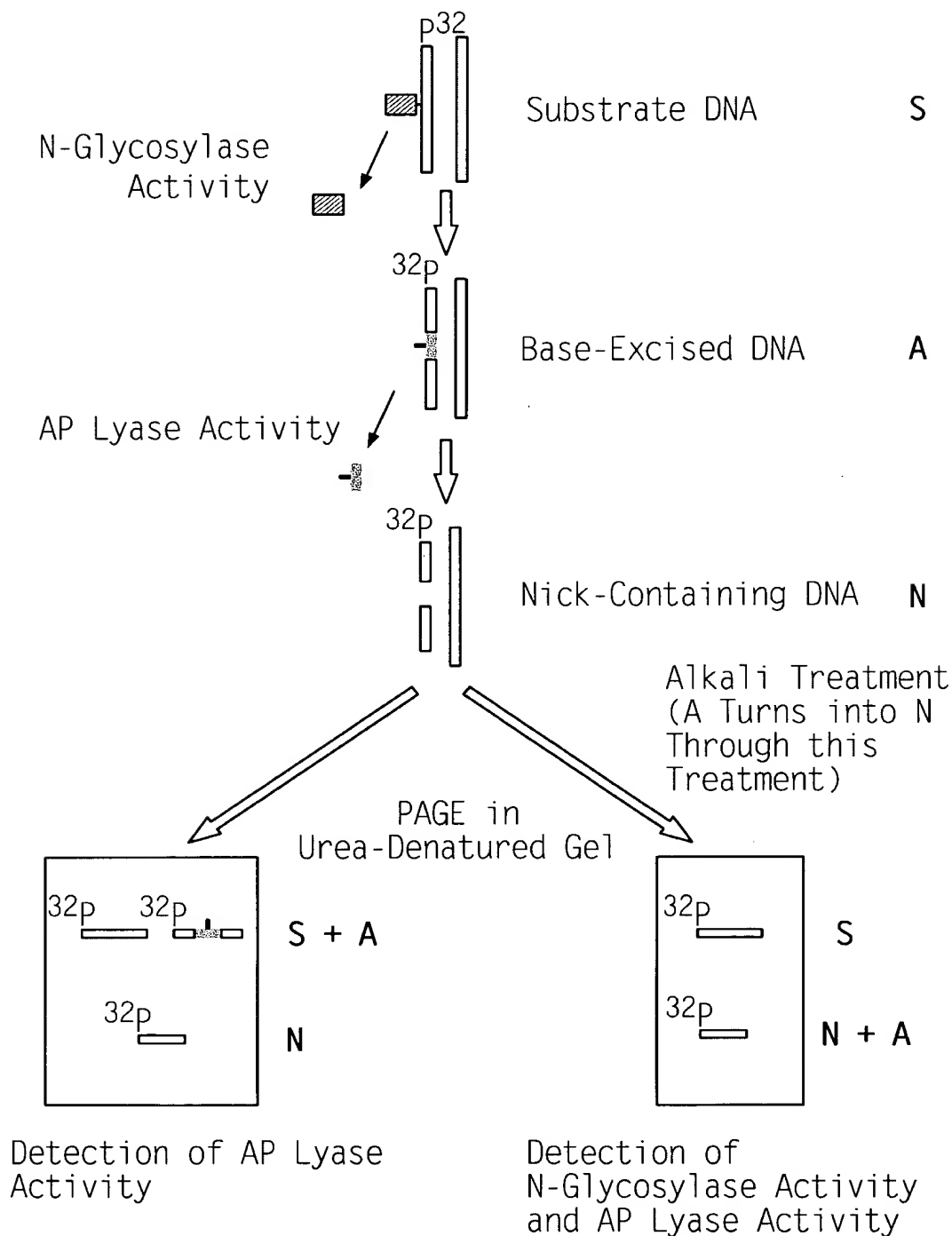


FIG. 6



7/36

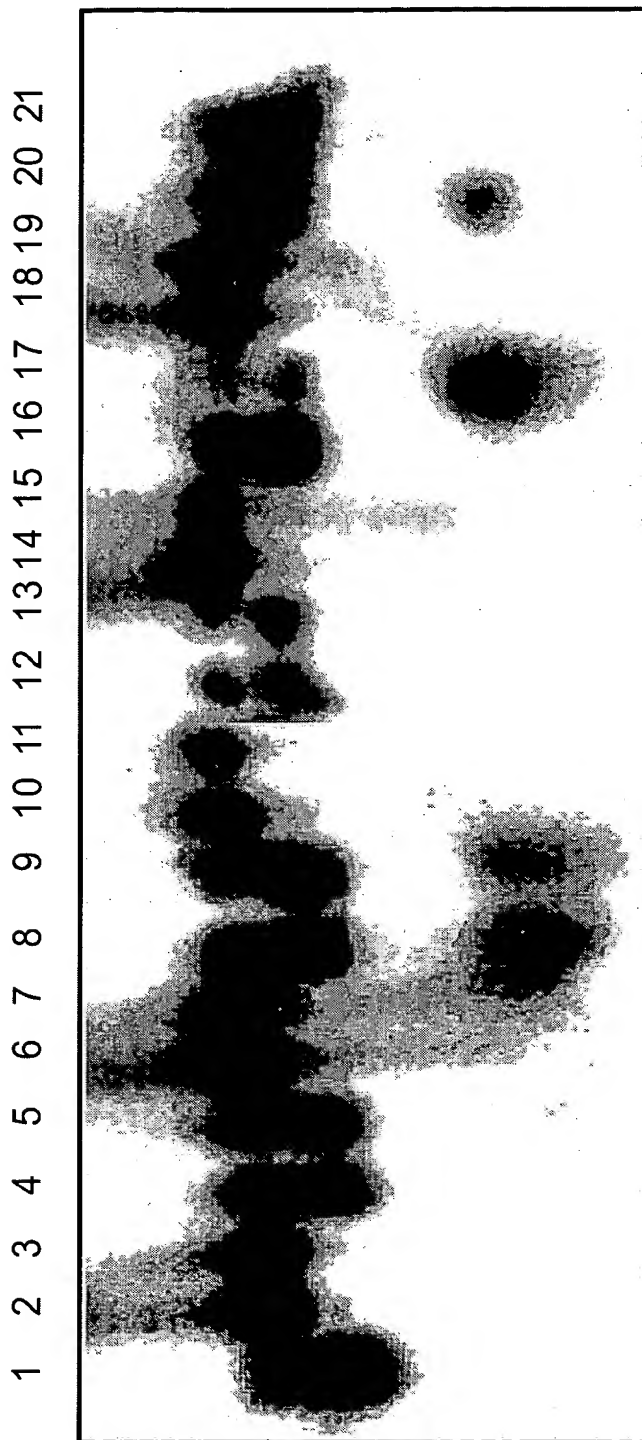
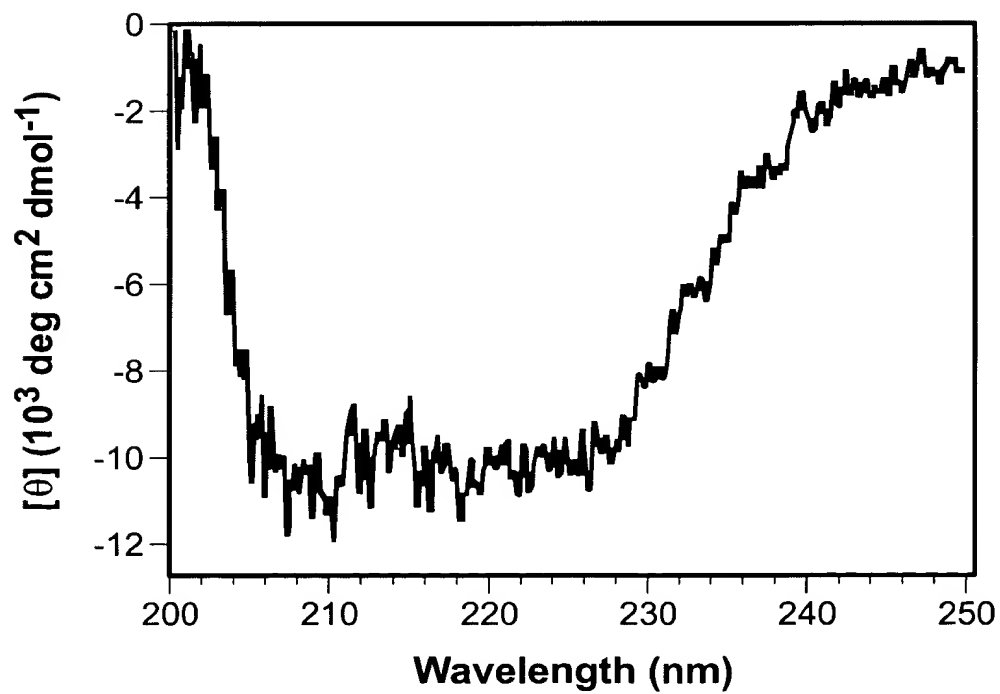
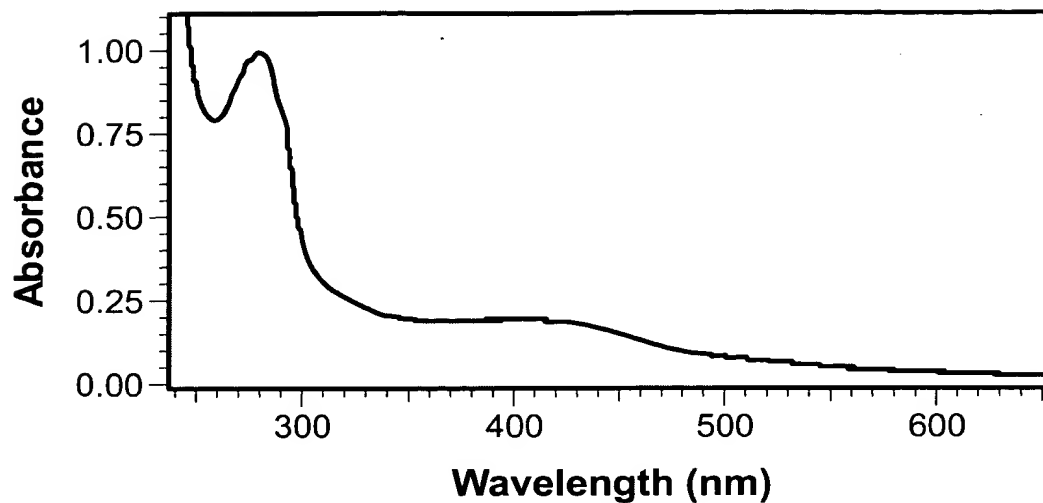


FIG. 7



8/36







9/36

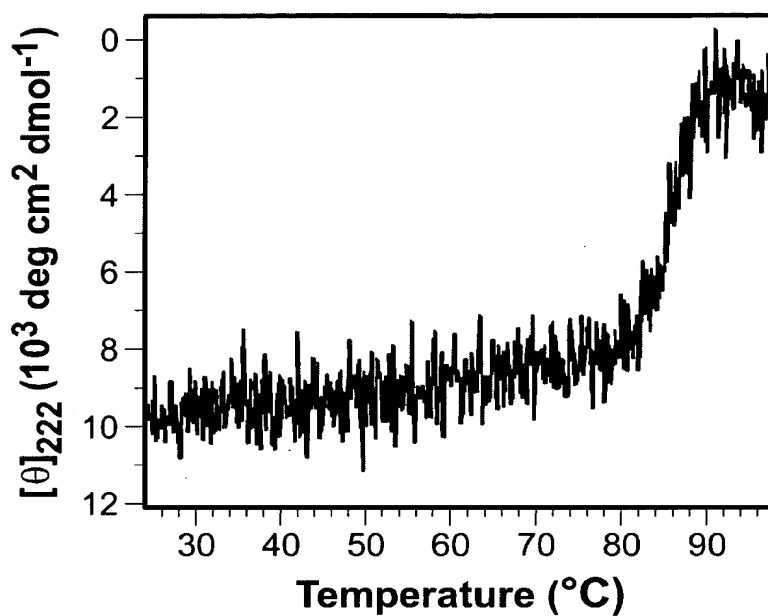


FIG. 10



10/36

5' - [<sup>32</sup>P]AGATCTTGACGGGGAAAYCCGAATTCGGCGAACGTGGCGAG - 3'  
3' - AATCTAGAACTGCCCCCTTTXGGCTTAAGCCGCTTGCACCGCTCTT - 5'

X : GO, G, C, T      Y : A, G



Annealing

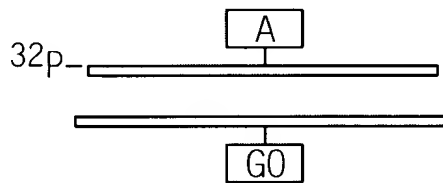
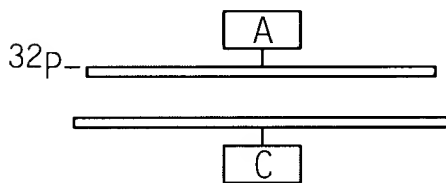
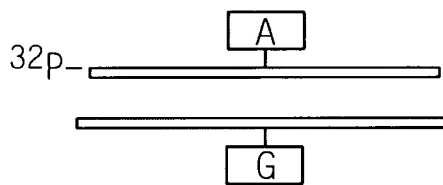
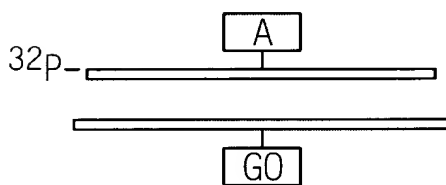
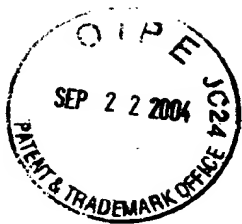


FIG. 11



11/36

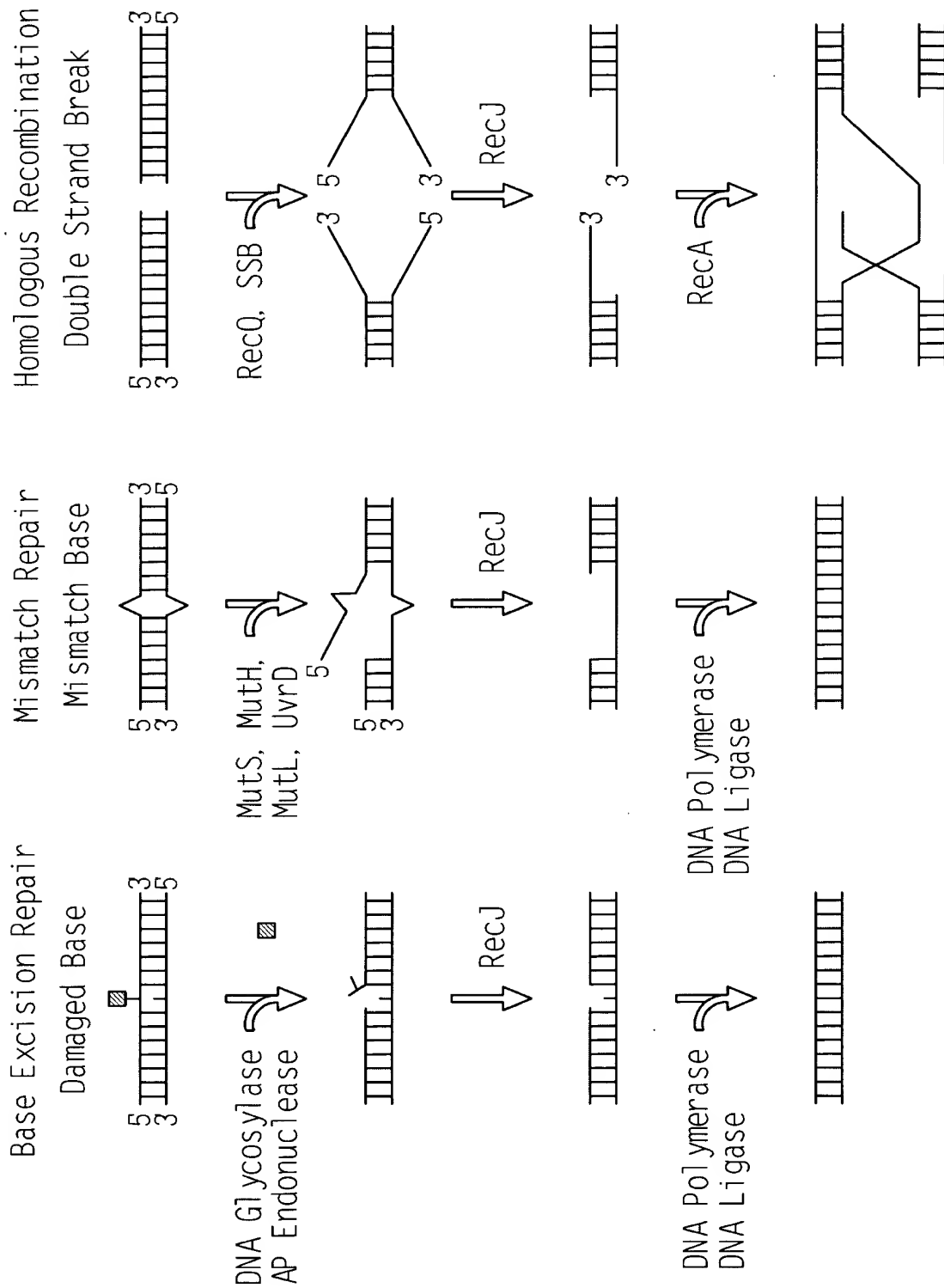


FIG. 12



12/36

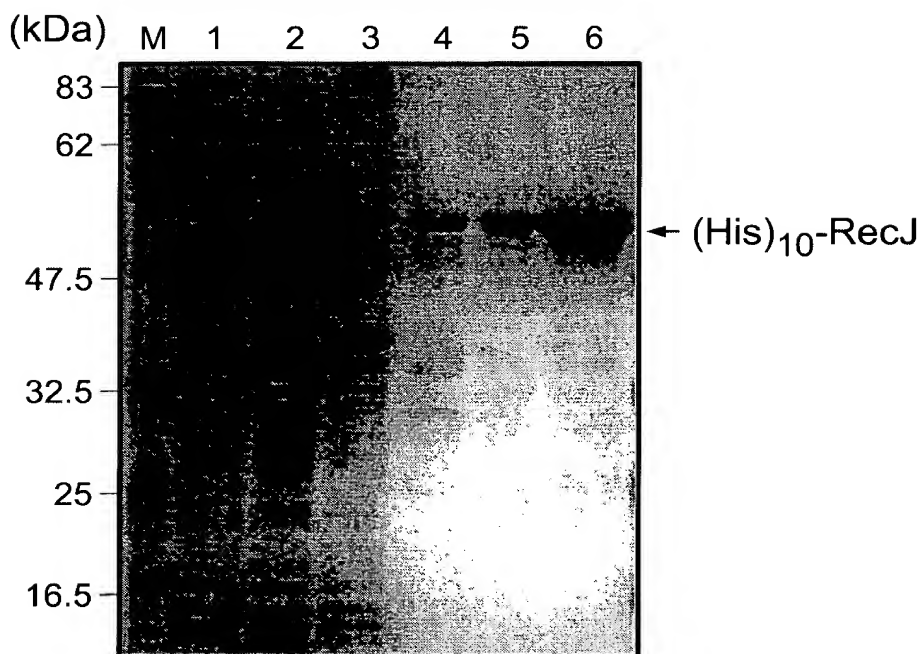
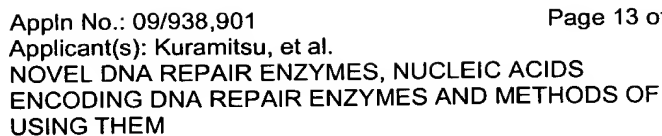


FIG. 13



13/36

## Motif I

RecJ_Tt	[73]	KRIIVHGDYDADGTTGTALIVRGLAALG	[100]
RecJ_Ec	[73]	TRIIIVGDFDADGATSTALSVLAMRSLG	[100]
RecJ_Aa	[78]	KRIIIYGDYDVGITGTALIVRVLKLLG	[105]
RecJ_Hp	[47]	TEILVVGDYDADGWISSAIMAKFFESLN	[74]
RecJ_Hi	[68]	QKIVIVGDFDADGATSTALSVLALRQLG	[95]

PPX1\_Sc [30] T T C V G N E S A D M D S I A S A T T T Y S C Q Y I Y N [57]  
PRUNE\_Dm [37] H L V M G N E S C D L D S A V S A V T L A F V Y A A S S [60]

Motif II

RecJ_Tt	[129]	SDLFLITVDCGITNHAELRE	[147]	[153]	VEVIVITPHHTPGK	[165]
RecJ_Ec	[131]	AQLIVITVDNGISSHAGVEH	[49]	[155]	IPVIVITPHHLPDG	[165]
RecJ_Aa	[133]	GDFLITVDNGTSAVEEIDQ	[151]	[154]	LETVVITPHHNVP	[166]
RecJ_Hp	[102]	APLIITVDNGINAFEAARF	[120]	[126]	YTLIITPHHCLHH	[138]
RecJ_Hi	[126]	VQLLMTVDNGVSSFDGVA	[144]	[150]	IRVLVITPHHLPPE	[162]

PPX1\_Sc [120] ELNSYLVDINNDTPKNLKNY [138] [141] NVVGIIIDHFDLQ [153]  
PRUNE\_Dm [88] PLVCEIMWDCRARVALPRRY [106] [129] NVTEILDHRLPED [141]

Motif IV

RecJ_Tt	[210]	YADLAAVGTTADVAPLWGW	[228]	[386]	DLLLRYGGHKEAGFAM	[402]
RecJ_Ec	[226]	LLDLVALGTVDVPLDAN	[244]	[422]	GMMLKFGGHAMAAGLSL	[438]
RecJ_Aa	[215]	FLDLVALGLLADYMPVNPV	[233]	[404]	DMFLKWGGHDKAMGLTL	[420]
RecJ_Hp	[189]	LLCLAGVATIDMMPLTFF	[207]	[372]	SLLLYGGHRQACGLSV	[388]
RecJ_Hi	[219]	LLDLVALGTIDVPLDQN	[237]	[415]	NMILKFGGHAMAAGLSI	[431]

## Specific Motif

PPX1\_Sc [191] IALLMGATLIDTSNMRRK [209]  
PRUNE\_Dm [183] VAQLLHATIVLDTINFAPA [201]

Tt : *Thermus thermophilus* HB8, Ec : *Escherichia coli*, Aa : *Aquifex aeolicus*,  
Hp : *Helicobacter pylori*, Hi : *Haemophilus influenzae* Rd,  
Sc : *Saccharomyces cerevisiae*, Dm : *Drosophila melanogaster*

**FIG. 14**



14/36

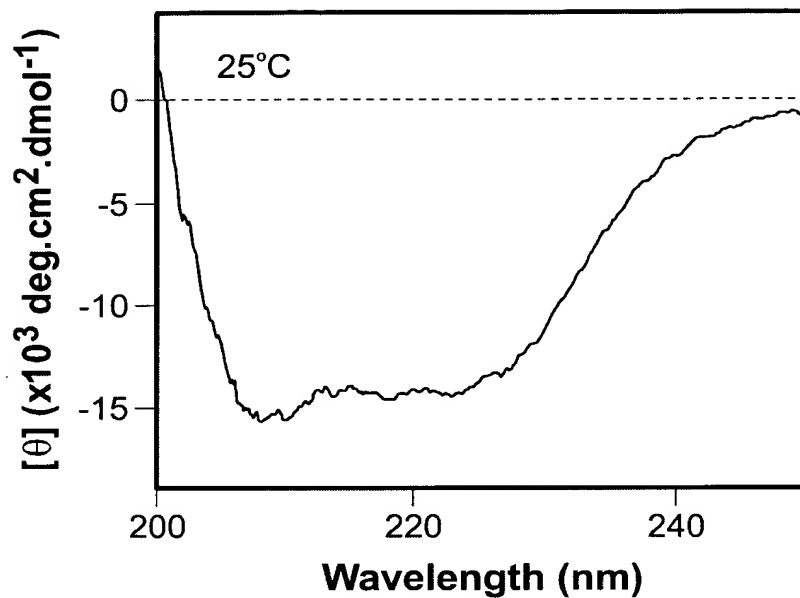


FIG. 15

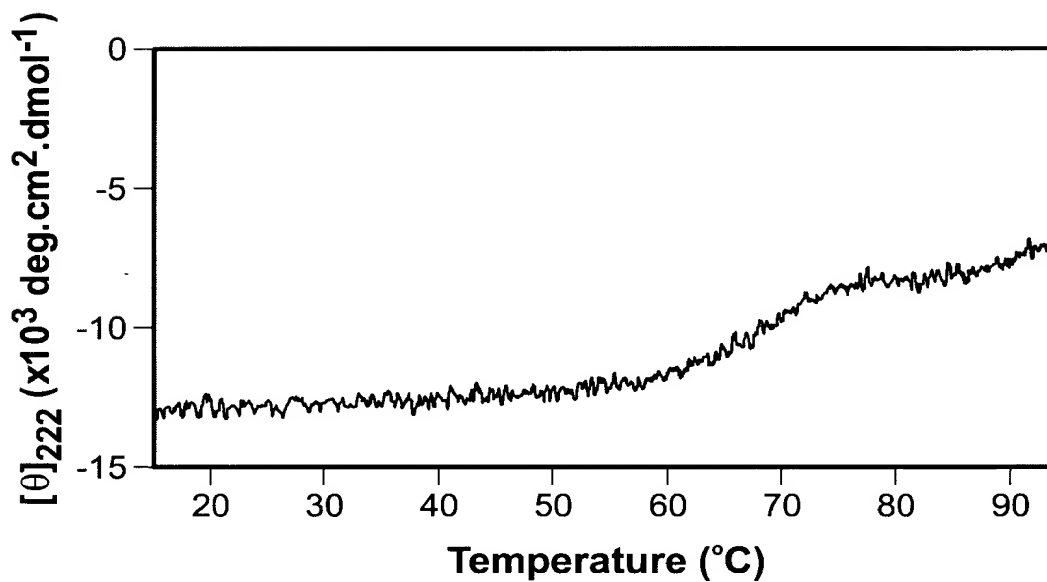


FIG. 16



15/36

Substrate DNA: 49' mer ssDNA

5' -ACTACTTGGTACACTGACGCGAGCACGCAGGAGCTCATTCCAGTGCGCA-3'

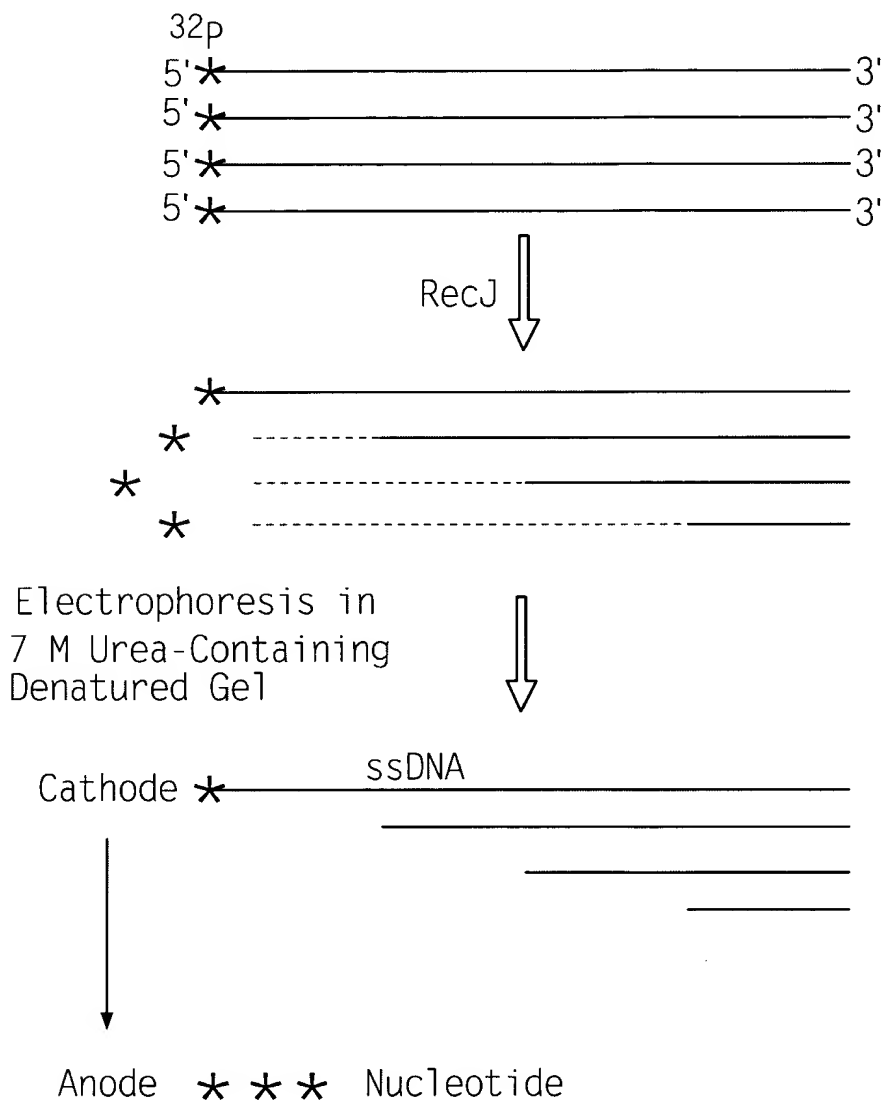


FIG.17



16/36

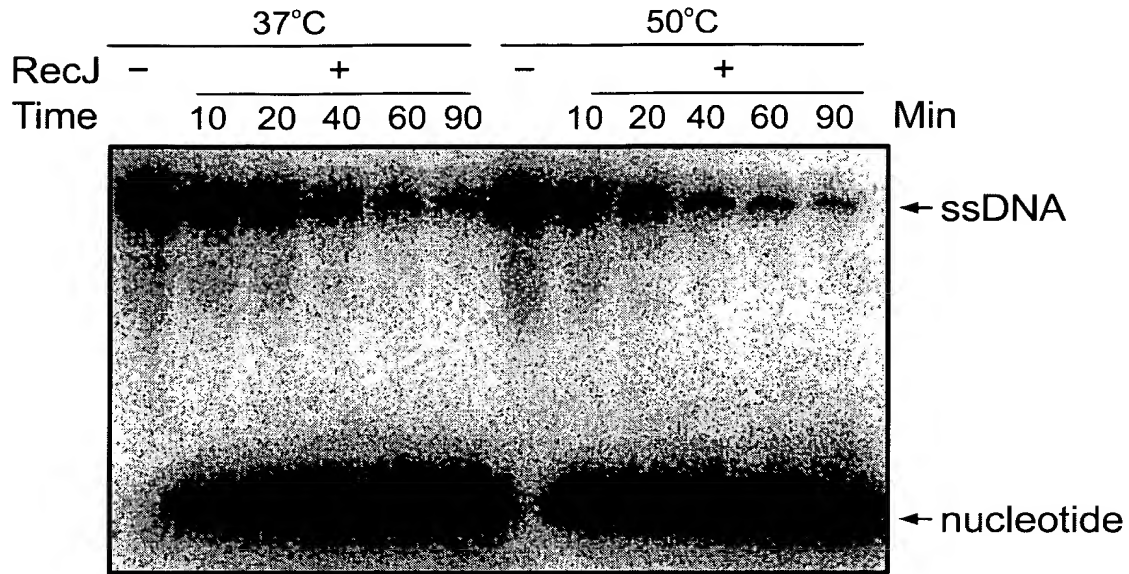


FIG. 18A

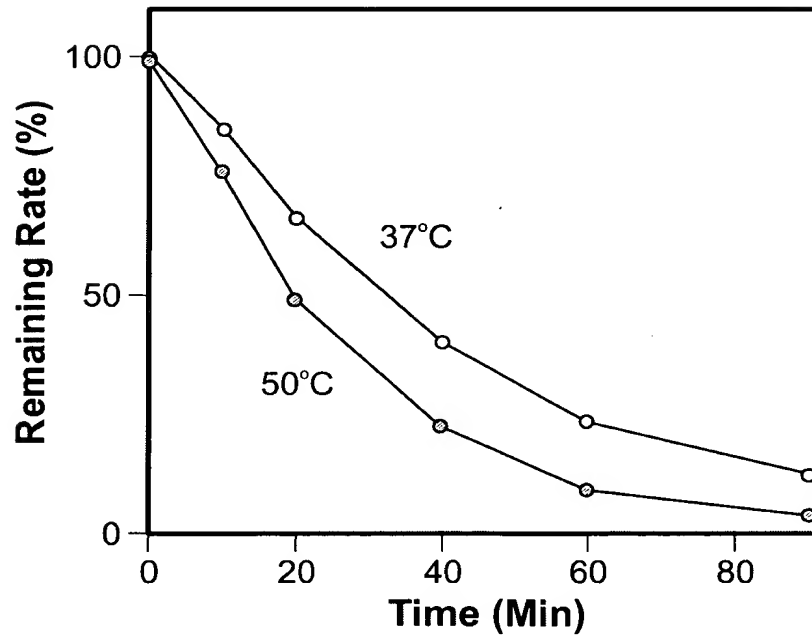
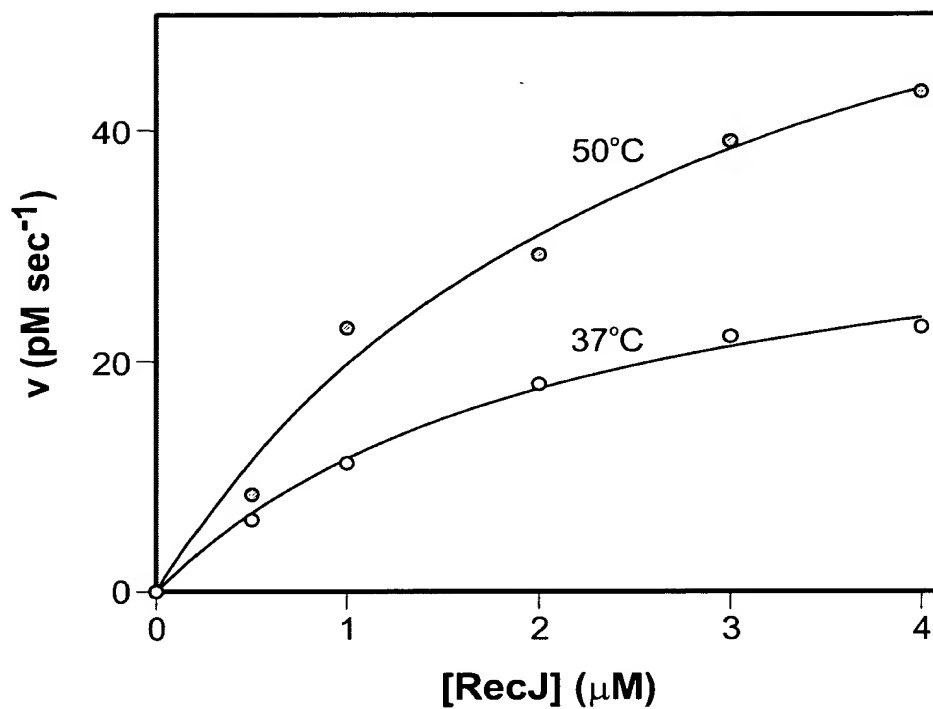


FIG. 18B



**17/36****FIG. 19**



18/36

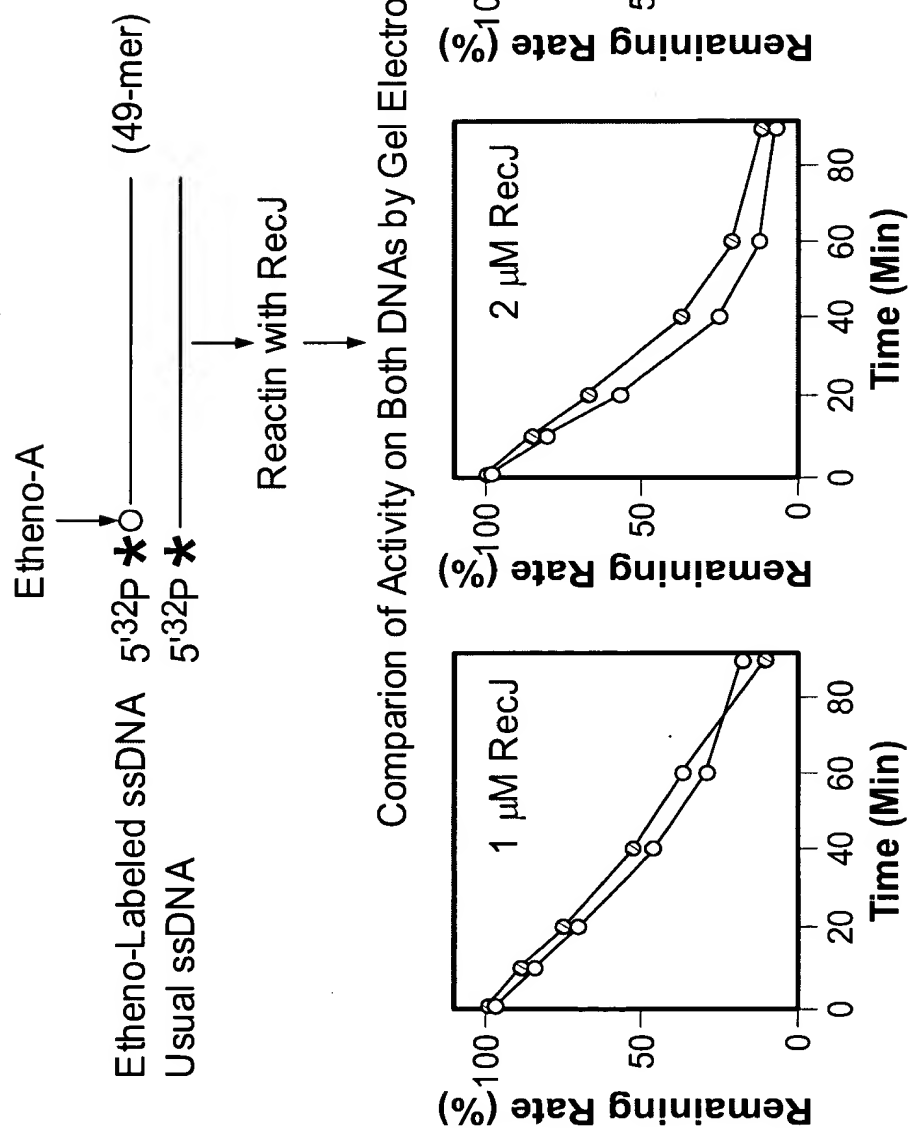


FIG. 20



19/36

**Substrate DNA : Etheno-Labeled Bovine Thymus  
ssDNA (e DNA)**

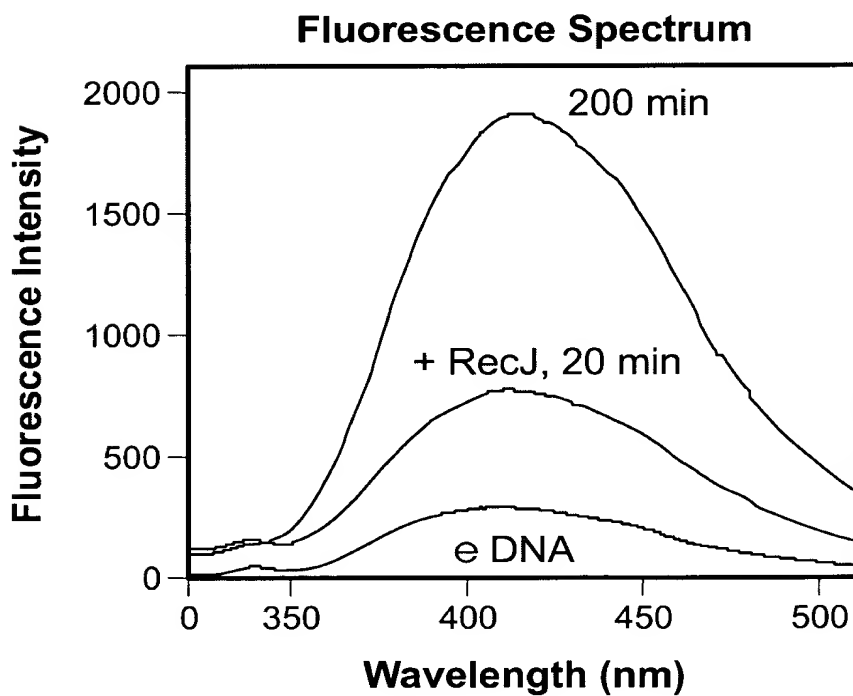
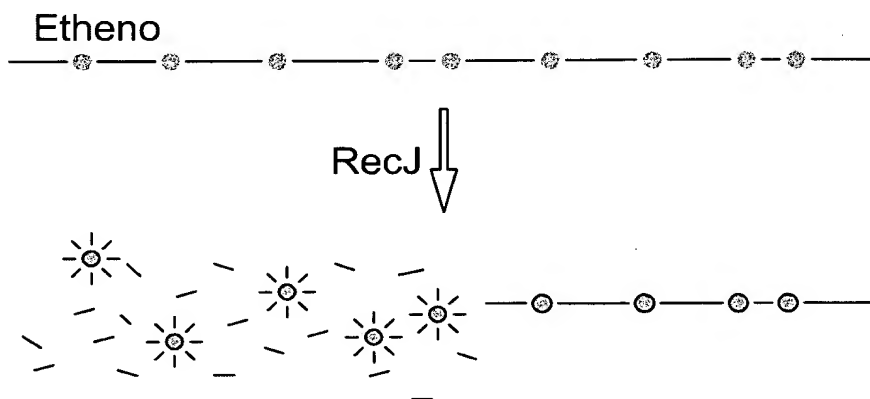
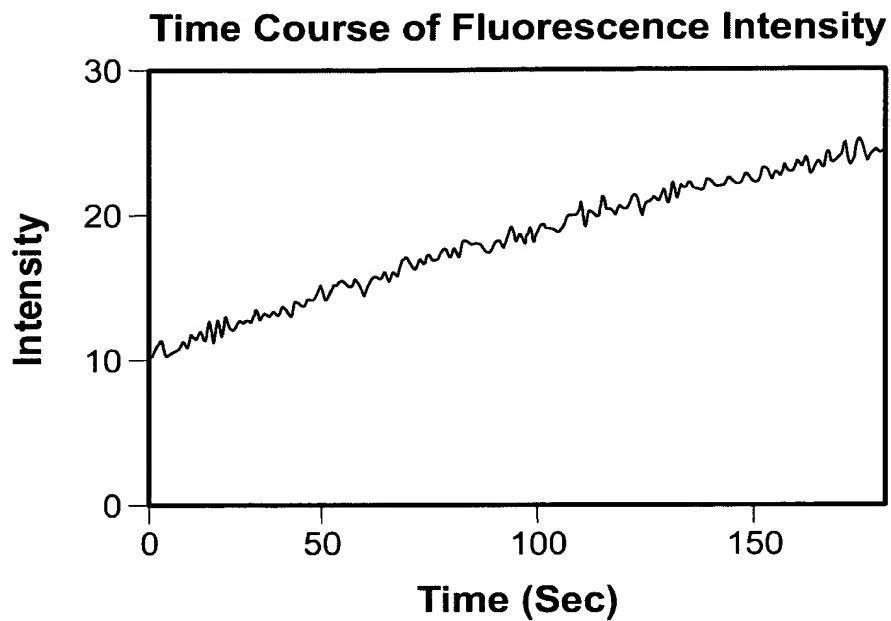


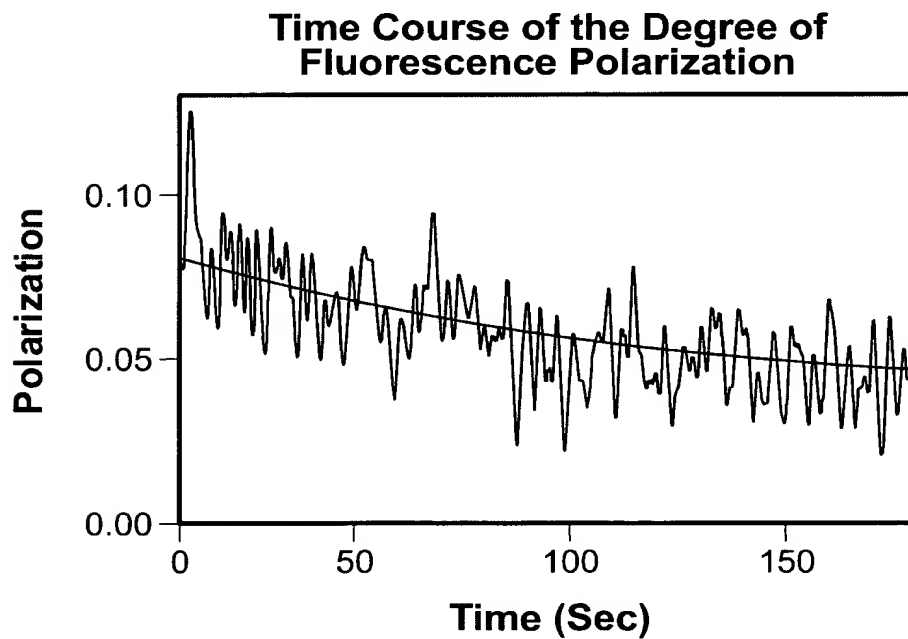
FIG. 21



20/36



**FIG. 22A**



**FIG. 22B**



21/36

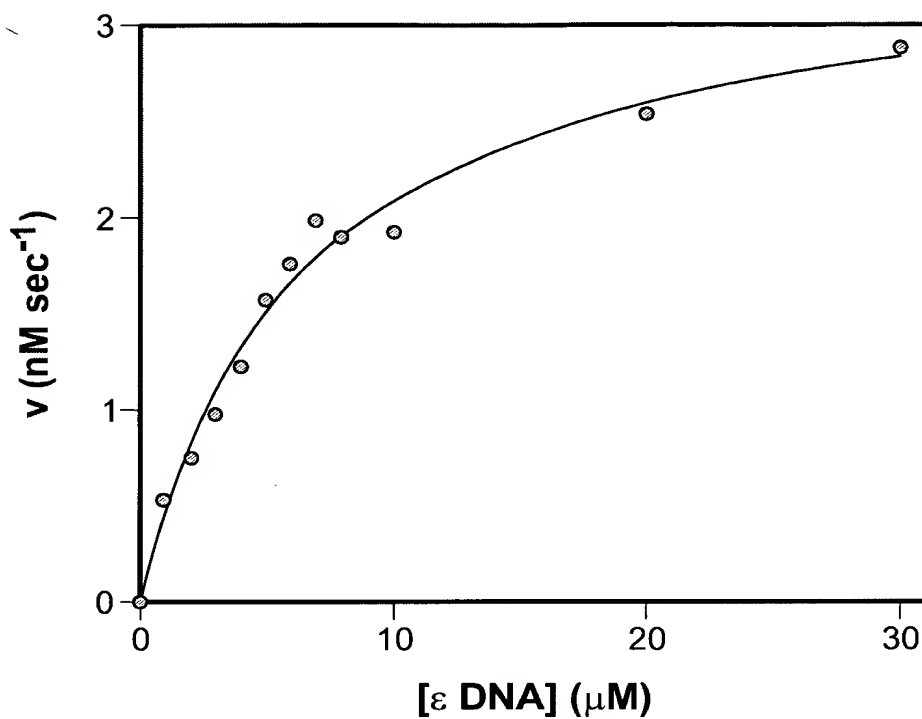
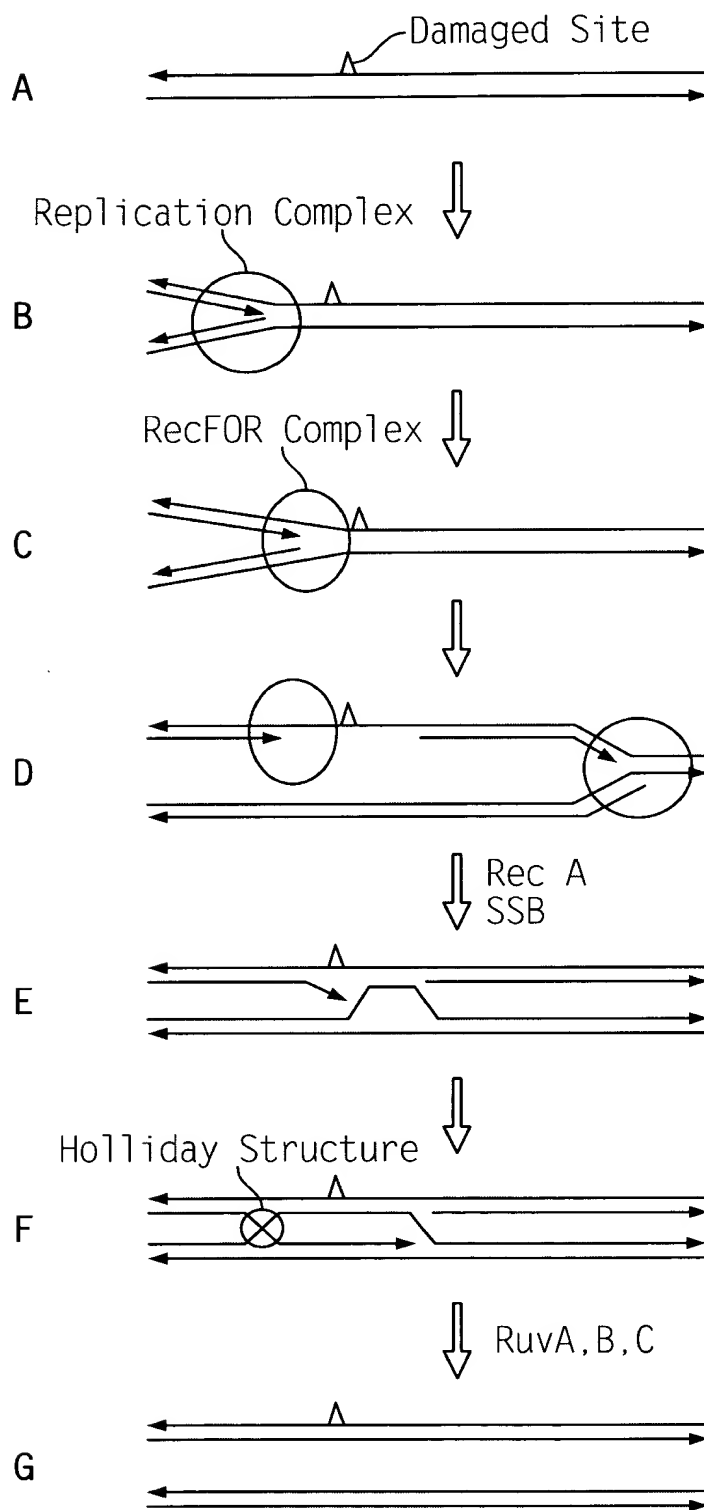


FIG. 23

**22/36****FIG. 24**



23/36

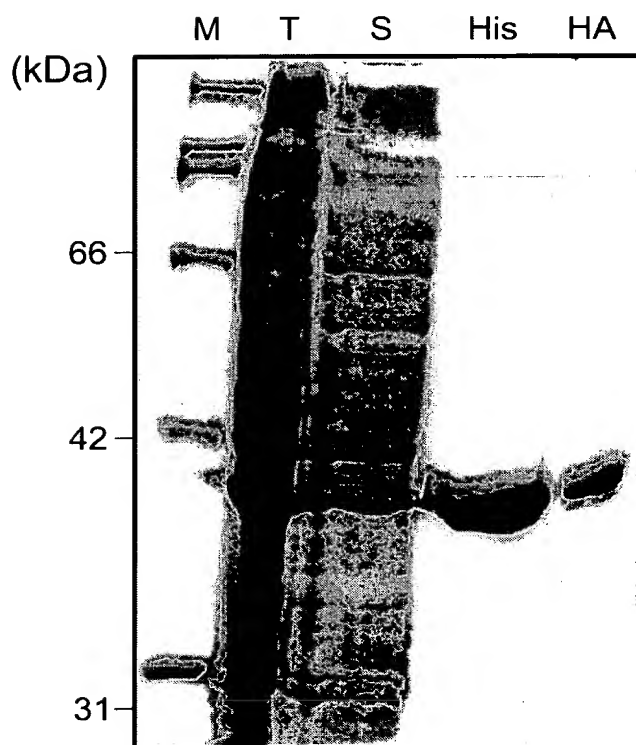


FIG. 25



24/36

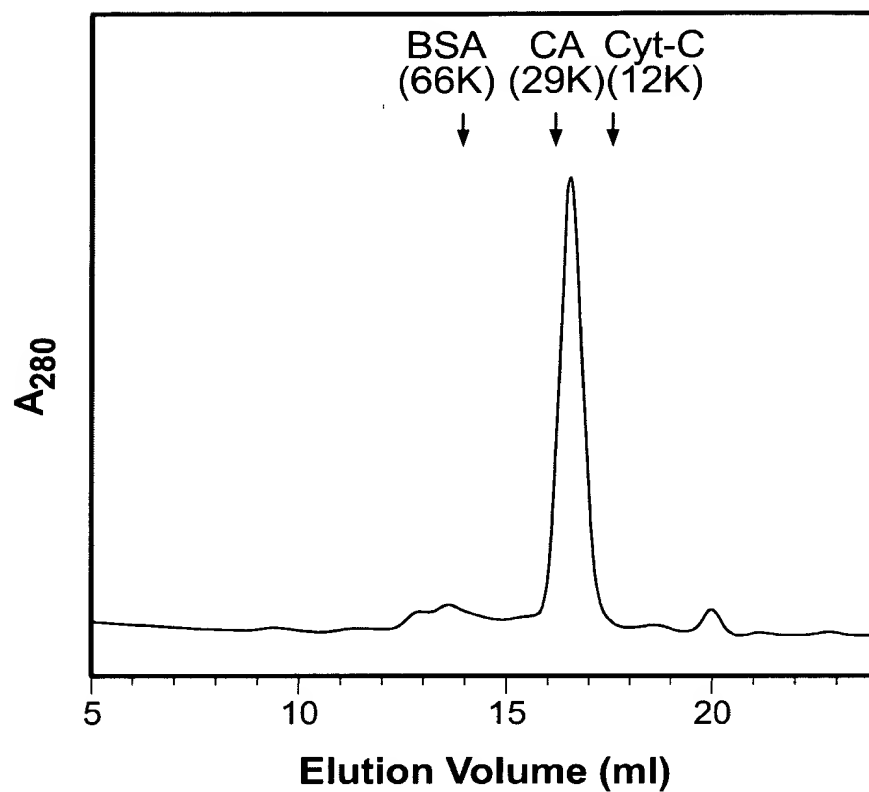


FIG. 26







26/36

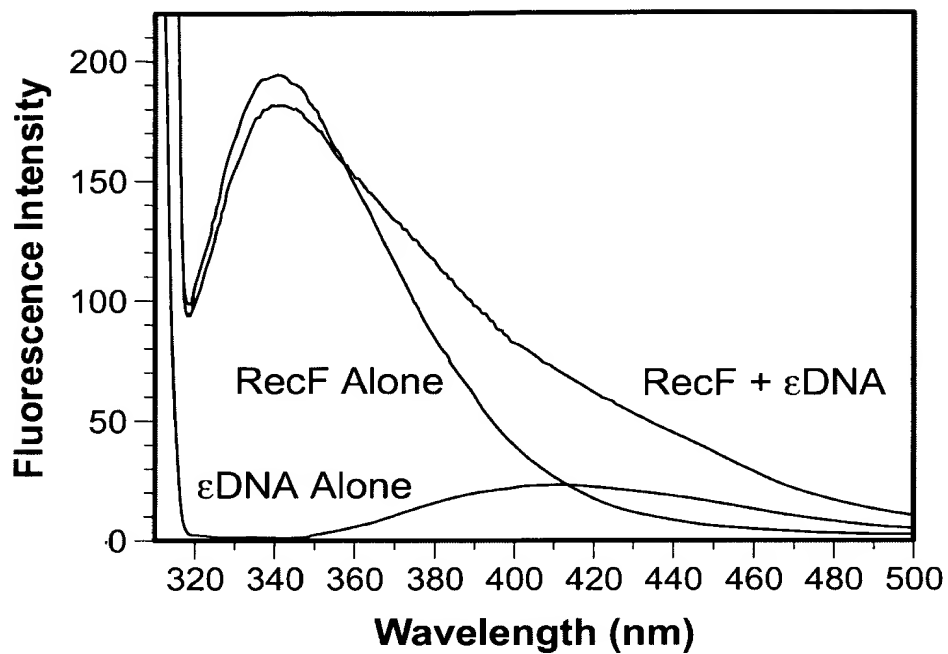


FIG. 28A

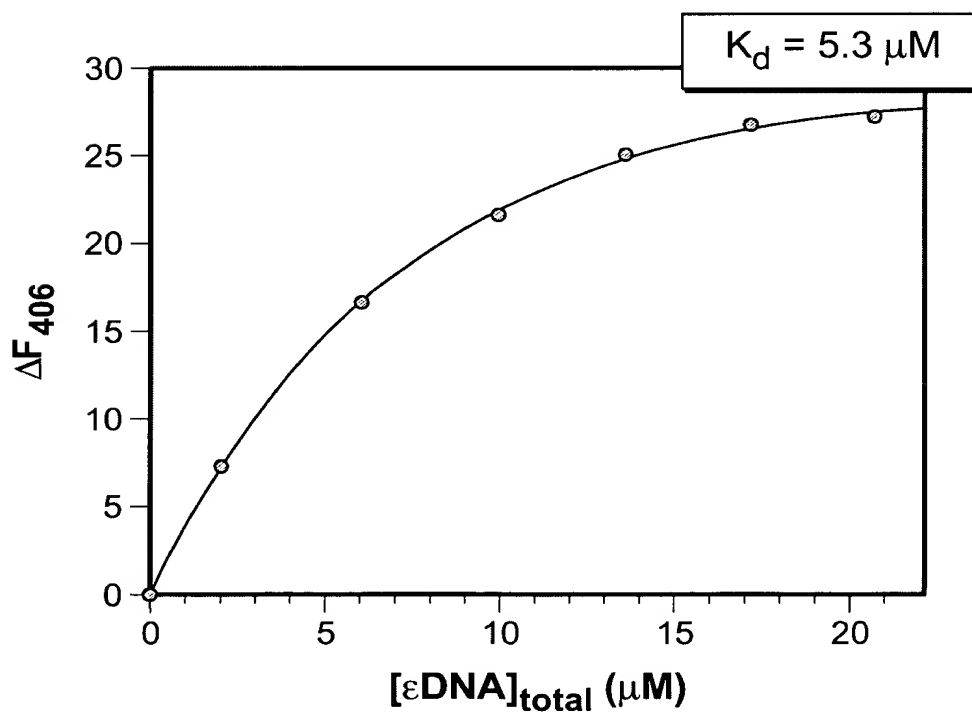


FIG. 28B



27/36

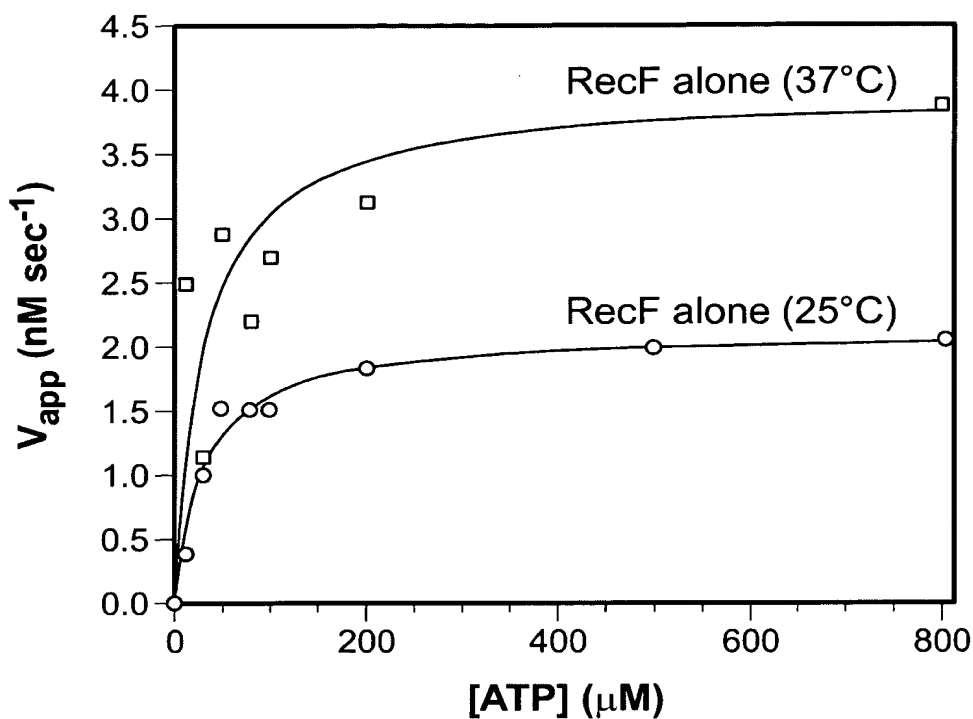


FIG. 29

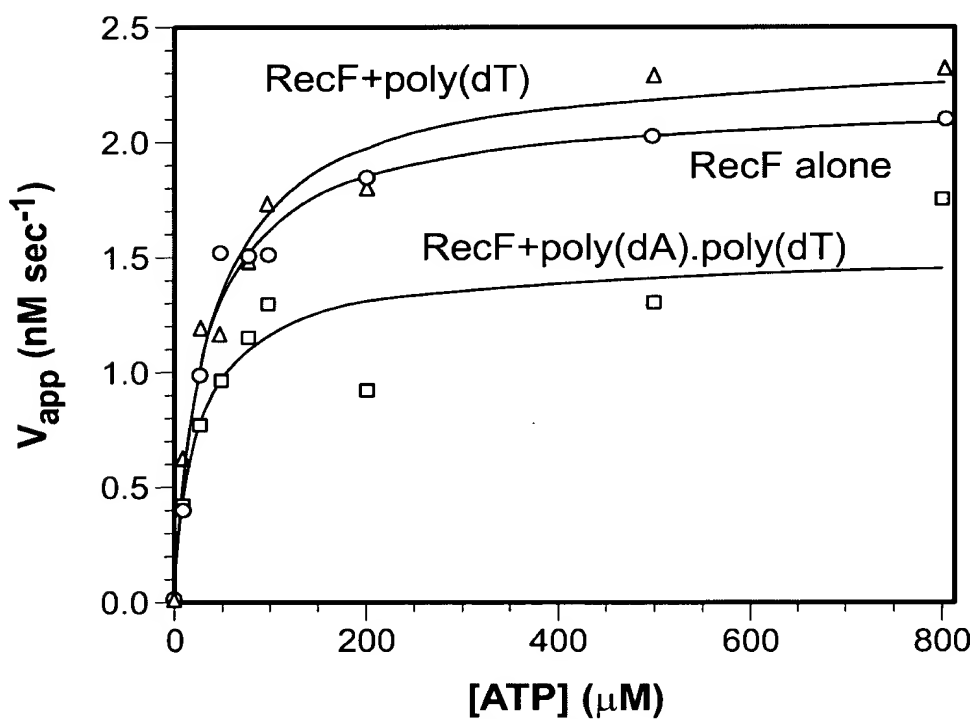


FIG. 30



28/36

Repair of Entire Genome

Transcription-Coupled  
Repair

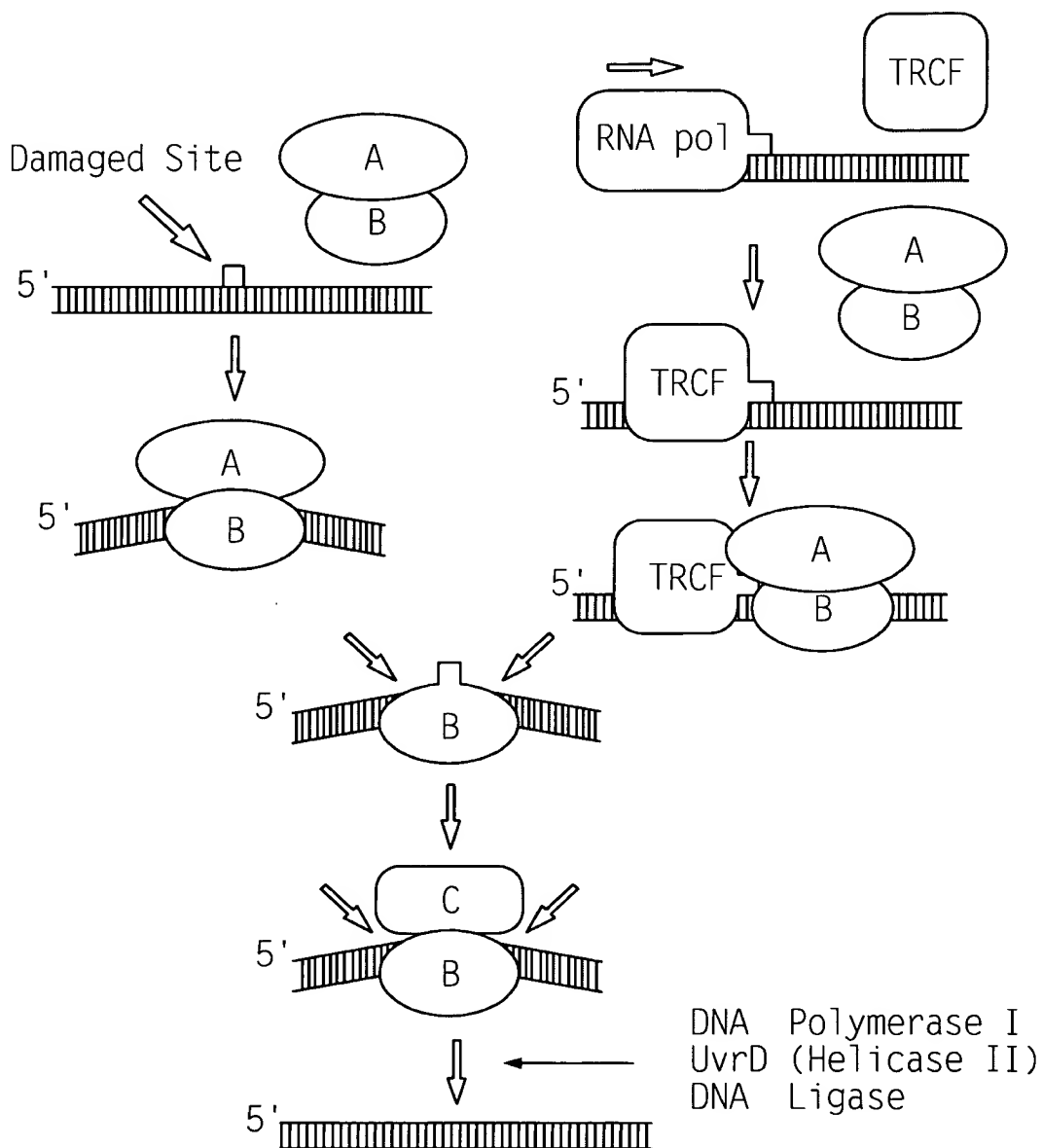


FIG. 31



29/36

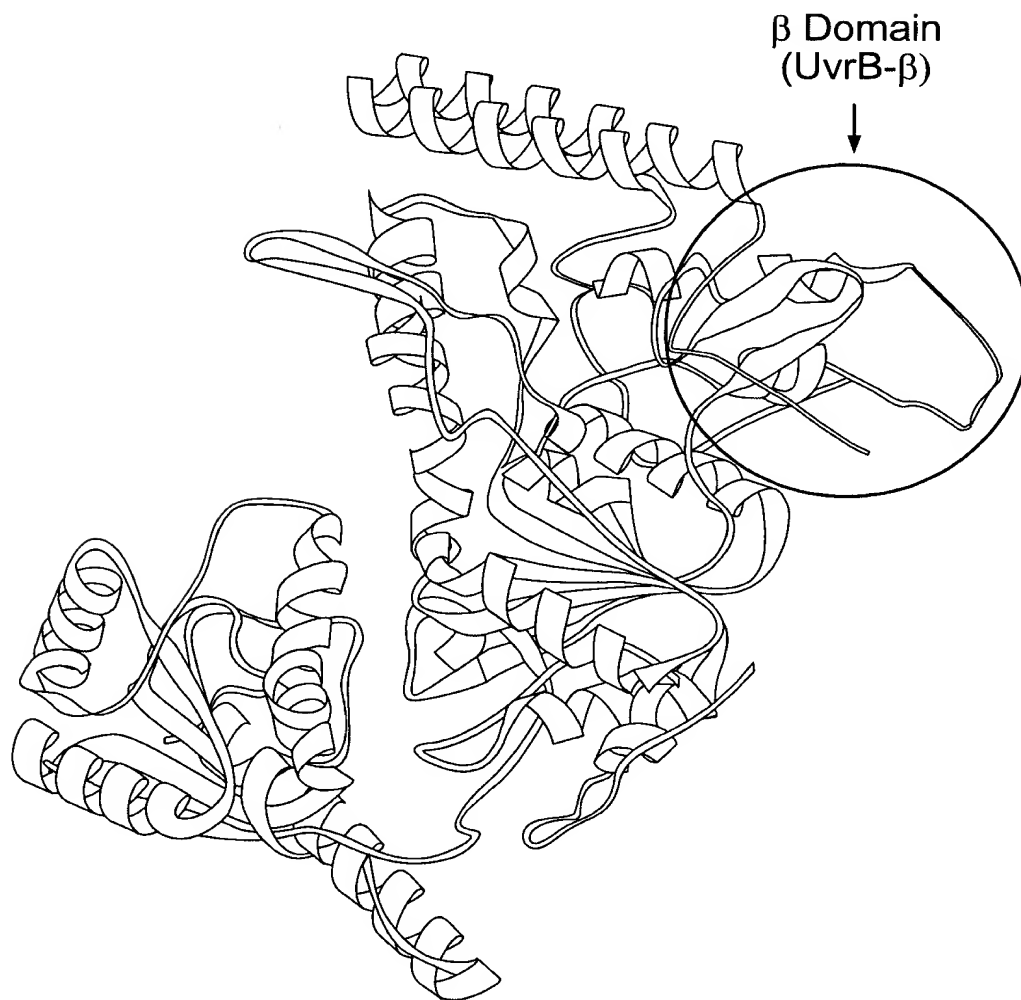


FIG. 32



30/36

UvrB- $\beta$

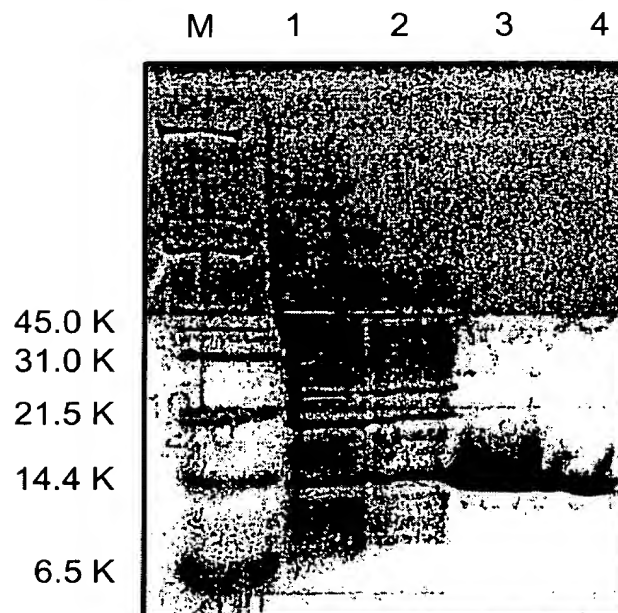


FIG. 33A

TRCF- $\beta$

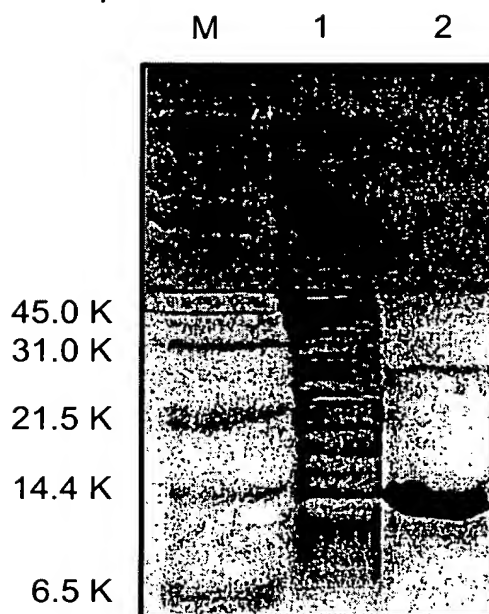


FIG. 33B



31/36

UvrB- $\beta$	154	RNLVVERGKPYPREVLLERLLELGYQRNDI	184
TRCF- $\beta$	86	WRLLLEVGRAYPREALLSRLLKLGYAR---	113
		* * * * *	

UvrB- $\beta$	185	DLSPGRFRKGEVLEIFPAYETETIRVELF	215
TRCF- $\beta$	114	DED---YRVLGEVVELG-----EVRLEFF	148
		* * * * *	

UvrB- $\beta$	216	GDEVERISQVHPVTG-ERLRELPG-----	236
TRCF- $\beta$	149	GDELERLVVRGEERRRHVLLPKPGKAEGFT	163
		* * * * *	

UvrB- $\beta$	237	---FVLFPA	242	*Identical Amino Acid Residues
TRCF- $\beta$	164	SKKVLFHPG	172	.Homologous Amino Acid Residues
		**		

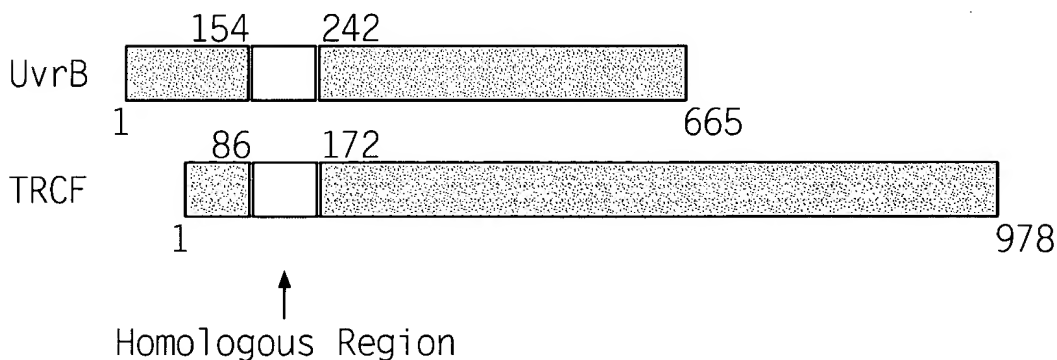


FIG. 34



32/36

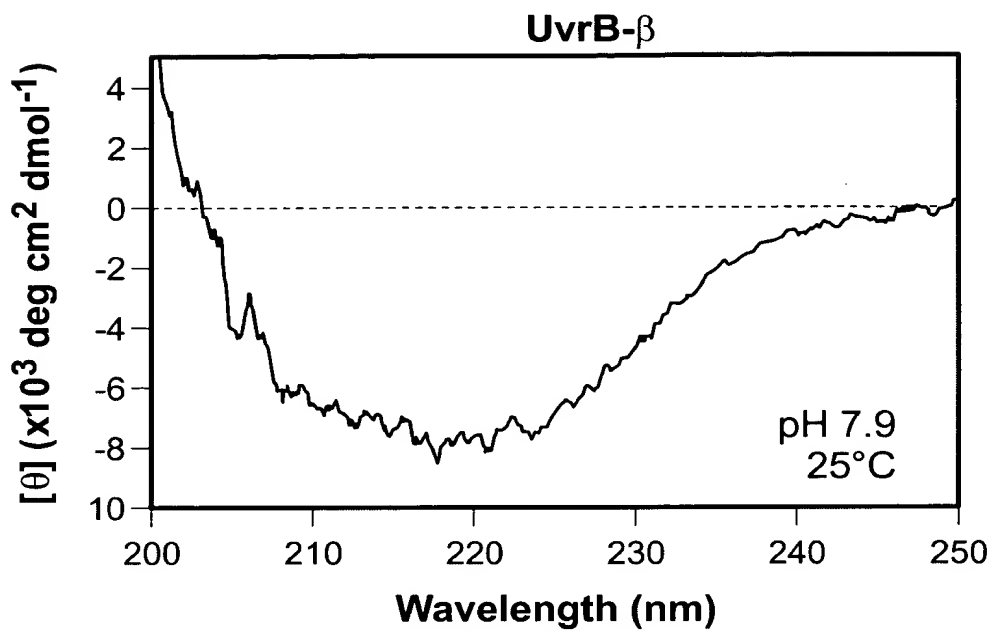


FIG. 35A

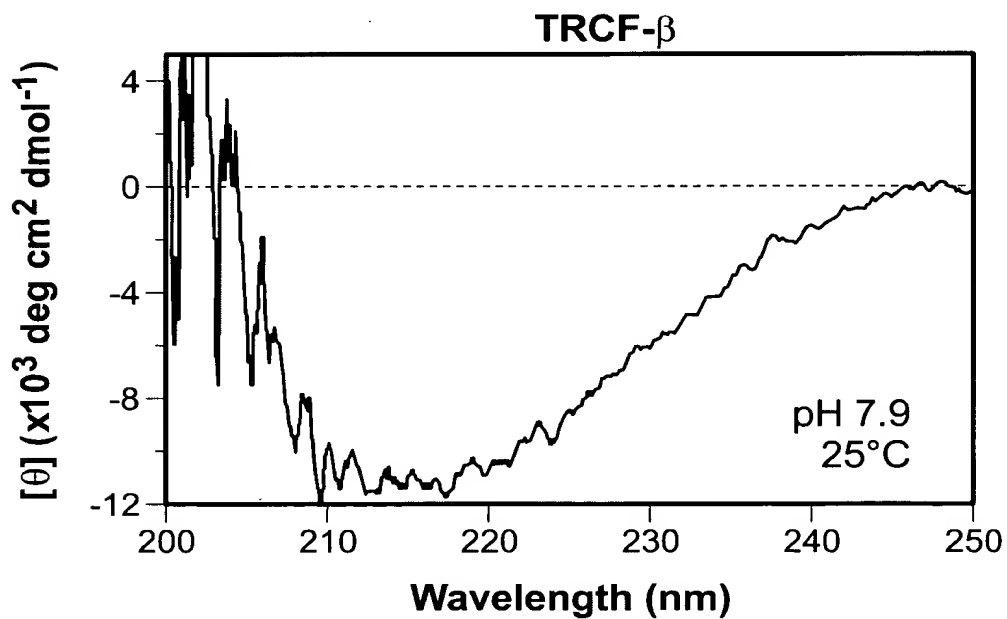


FIG. 35B





33/36

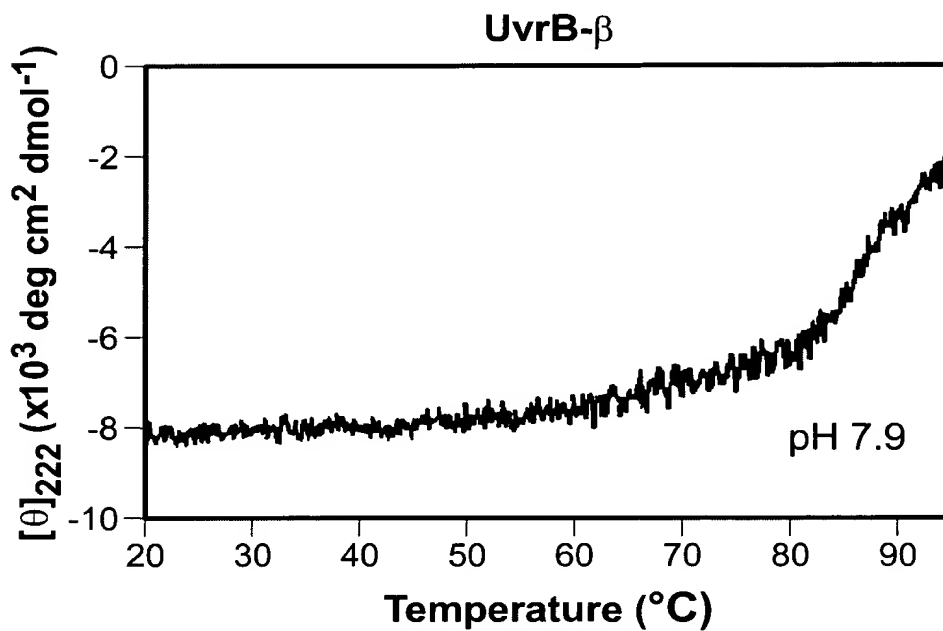


FIG. 36A

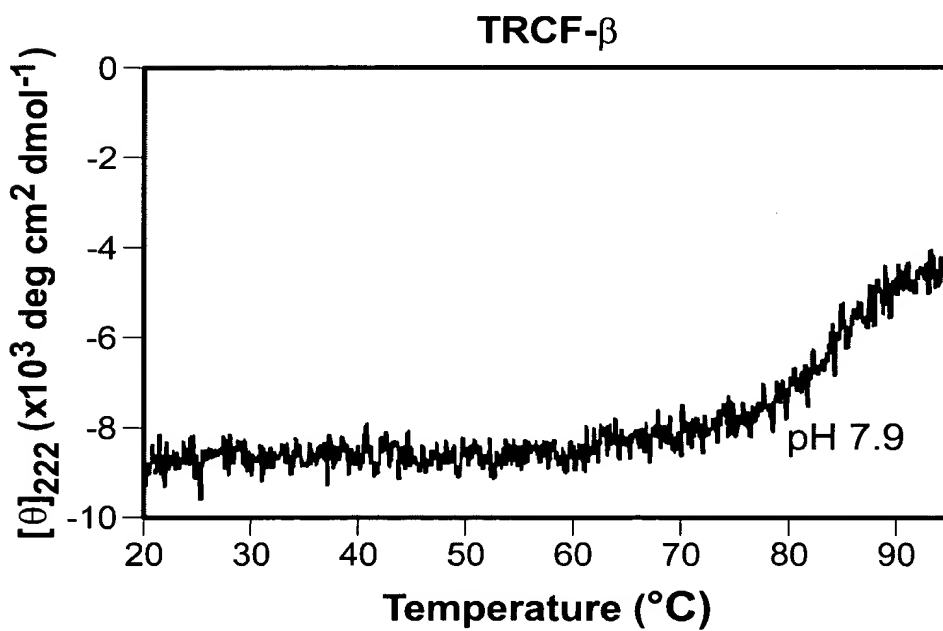
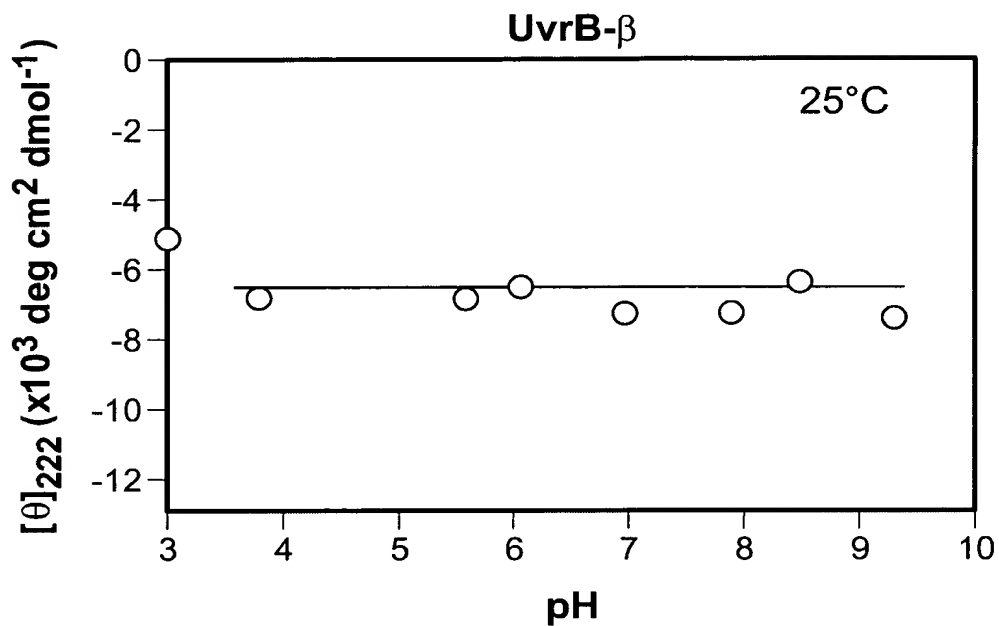


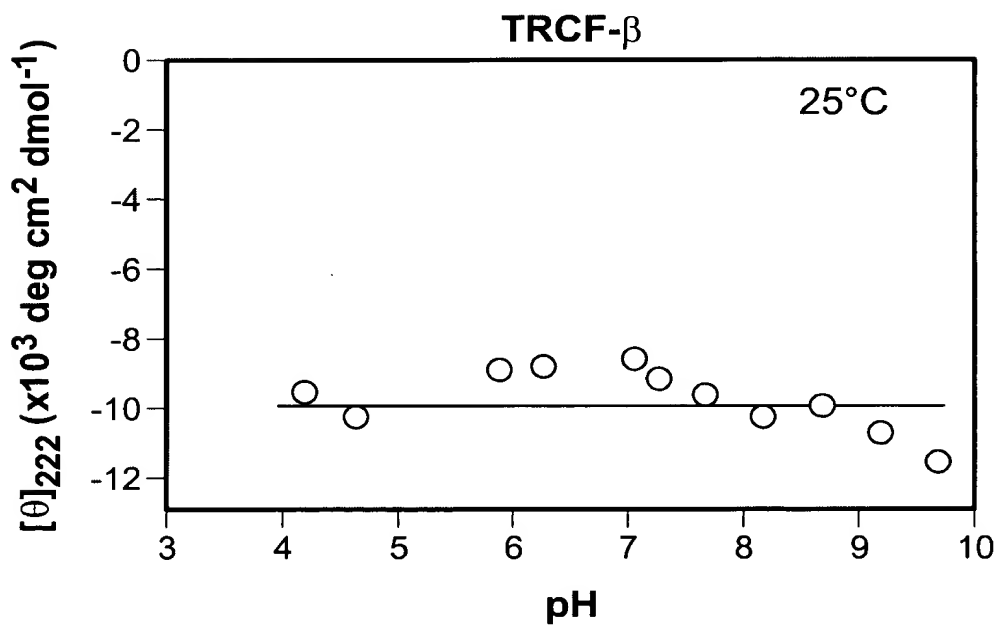
FIG. 36B



34/36



**FIG. 37A**



**FIG. 37B**

35/36

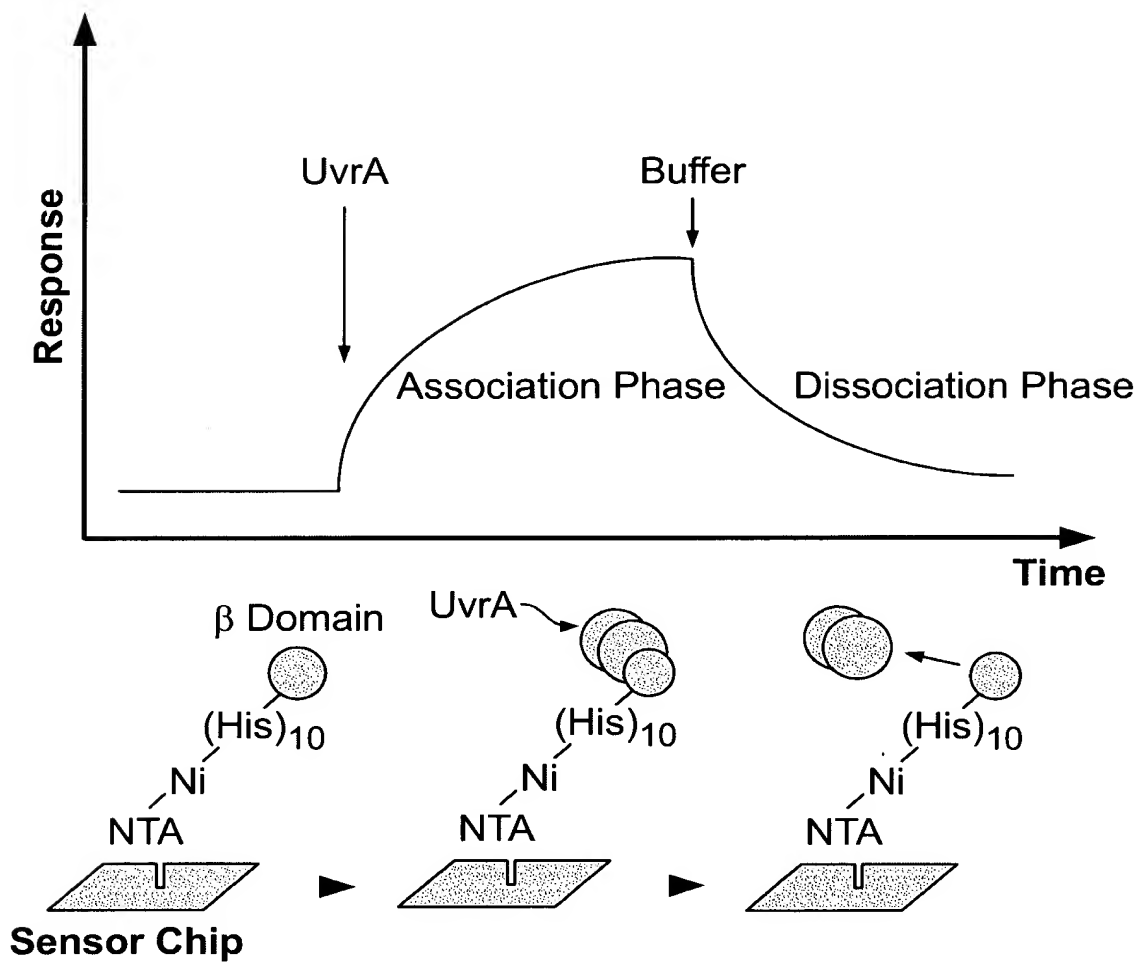
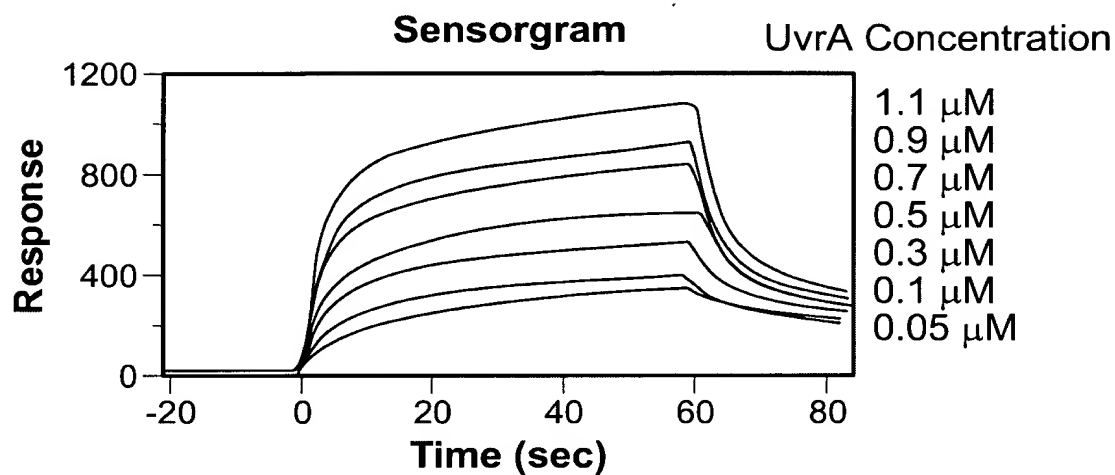


FIG. 38



36/36



**Analytical Results**

	$K_d$ ( $\times 10^{-6}M$ )		$k_{on}$ ( $\times 10^5 M^{-1}S^{-1}$ )		$k_{off}$ ( $\times 10^{-1}S^{-1}$ )	
	-ATP	+ATP	-ATP	+ATP	-ATP	+ATP
UvrB-b	2.6	0.4	2.0	1.5	5.2	0.6
TRCF-b	1.3	0.5	1.0	1.5	1.3	0.7

**FIG. 39**

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